Amendment to the Claims

1. (Currently amended) A method of ~~diagnosing an increased probability of~~ screening for breast cancer in a subject, the method comprising obtaining a sample containing cells from the subject, assaying the level of FLJ20174 nucleic acid, SEQ ID NO:3 or SEQ ID NO:4 or the full length complement of either thereof, comparing the ~~expression pattern~~ level of ~~CXCL9 or~~ FLJ20174 nucleic acid, SEQ ID NO:3 or SEQ ID NO:4 or the full length complement of either thereof, ~~or gene product~~ in ~~a~~ the sample from ~~a~~ the subject with the ~~expression pattern~~ level of ~~CXCL9 or~~ FLJ20174 nucleic acid, SEQ ID NO:3 or SEQ ID NO:4 or the full length complement of either thereof, ~~or gene product~~ in one or more control samples from one or more non-cancerous breast tissues, wherein ~~an upregulation~~ a significant increase in the ~~expression pattern of CXCL9 or~~ level of FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 or the full length complement of either thereof, in the subject sample compared to the control samples is indicative of ~~an increased probability of~~ breast ~~or ovarian~~ cancer in the subject and wherein assaying the level comprises an amplification step.

2. (Canceled)

3. (Currently amended) The method of claim ~~2~~ 1, wherein the one or more control breast tissue samples from a non-cancerous breast tissue are also derived from the subject.

4. (Canceled)

5. (Currently amended) The method of claim [[4]] 1, wherein the difference in the ~~expression pattern~~ level is an ~~upregulation~~ increase of at least two fold over the level of ~~expression of CXCL9 or~~ FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 or the full length

complement of either thereof, nucleic acid in the one or more non-cancerous breast tissue samples.

6. (Canceled)

7. (Currently amended) The method of claim [[6]] 1, wherein the cells are obtained from breast ~~or ovarian~~ tissue.

8. (Currently amended) The method of claim 1, wherein the subject sample comprises serum, nipple aspirate or ductal fluid obtained from the subject.

9. (Currently amended) The method of claim 1, wherein the ~~expression pattern~~ level of ~~CXCL9 or~~ FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 or the full length complement thereof is determined by ~~detecting the presence in~~ assaying the sample ~~of a nucleic acid comprising~~ with a probe or primer consisting of 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous nucleotides of ~~SEQ ID NO:1~~ SEQ ID NO:3 or SEQ ID NO:4, or the full length complement thereof.

10-65. (Canceled)

66. (Currently amended) The method of claim [[9]] 1, wherein the step of assaying comprises a polymerase chain reaction step.

67. (Currently amended) The method of claim [[9]] 1, wherein the step of assaying comprises a reverse transcriptase polymerase chain reaction step.

68. (Currently amended) The method of claim [[9]] 1, wherein the step of assaying comprises a DNA to DNA hybridization step.

69. (Currently amended) The method of claim [[9]] 1, wherein the step of assaying comprises a DNA to RNA hybridization step.

70. (Cancel)

71. (Currently amended) The method of claim [[9]] 1, wherein the step of assaying wherein the probe is affixed to a solid support.

72. (Previously presented) The method of claim 71, wherein the solid support is a membrane, a microtiter plate, or a polystyrene bead.

73-74. (cancel)